

117: qb_cst148: *
118: qb_cst149: *
119: qb_cst150: *
120: qb_cst151: *
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124: qb_cst155: *
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127: qb_cst158: *
128: qb_cst159: *
129: qb_cst160: *
130: qb_cst161: *
131: qb_cst162: *
132: qb_cst163: *
133: qb_cst164: *
134: qb_cst165: *
135: qb_cst166: *
136: qb_cst167: *
137: qb_cst168: *
138: qb_cst169: *
139: qb_cst170: *
140: qb_cst171: *
141: qb_cst172: *
142: qb_cst173: *
143: qb_cst174: *
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148: qb_cst179: *
149: qb_cst180: *
150: qb_cst181: *
151: qb_cst182: *
152: qb_cst183: *
153: qb_cst184: *
154: qb_cst185: *
155: qb_cst186: *
156: qb_cst187: *
157: qb_cst188: *
158: qb_cst189: *
159: qb_cst190: *
160: qb_cst191: *
161: qb_cst192: *
162: qb_cst193: *
163: qb_cst194: *
164: qb_cst195: *
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166: qb_cst197: *
167: qb_cst198: *
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169: qb_cst200: *
170: qb_cst201: *
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172: qb_cst203: *
173: qb_cst204: *
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181: qb_cst212: *
182: qb_cst213: *
183: qb_cst214: *
184: qb_cst215: *
185: qb_cst216: *
186: qb_cst217: *
187: qb_cst218: *
188: qb_cst219: *
189: qb_cst220: *

190: qb_cst110: *
191: qb_cst111: *
192: qb_cst112: *
193: qb_cst113: *
194: qb_cst114: *
195: qb_cst115: *
196: qb_cst116: *
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198: qb_cst118: *
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206: qb_cst126: *
207: qb_cst127: *
208: qb_cst128: *
209: qb_cst129: *
210: qb_cst130: *
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217: qb_cst137: *
218: qb_cst138: *
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222: qb_cst142: *
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225: qb_cst145: *
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248: qb_cst168: *
249: qb_cst169: *
250: qb_cst170: *
251: qb_cst171: *
252: qb_cst172: *
253: qb_cst173: *
254: qb_cst174: *
255: qb_cst175: *
256: qb_cst176: *
257: qb_cst177: *
258: qb_cst178: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/lab-host="DH10B"
 /note="Origin: placenta; Vector: pRTTpac; Site 1: EcorI;
 Site 2: NotI. The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Honaido, M.F., Lennon, G. and Soares,
 M.B. (1996). Genome Research 6(9): 791-806."

BASE COUNT 160 a 111 c 141 g 124 t

ORIGIN

Query Match 33.0%; Score 534.4; DB 143; Length 536;
 Best Local Similarity 99.8%; Pred. No. 2.5e-126;
 Matches 531; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 545 acagcccaagaagctcttctgttgatatacccatcaagaaccagaagttgttgca 604
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 acagcccaagaagctcttctgttgatatacccatcaagaaccagaagttgttgca 60
 QY 605 gcaagcattcaagaagctcttctgttgatatacccatcaagaag 664
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 gcaagcattcaagaagctcttctgttgatatacccatcaagaag 120
 QY 665 atgagacataaagcagaagaagaagaagaagaagaagaagaagaagaagaat 724
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 atgagacataaagcagaagaagaagaagaagaagaagaagaagaagaagaat 180
 QY 725 cggactggttcaacccatttaaacgccccgaggttgagacatgagaagtgagctc 784
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 cggactggttcaacccatttaaacgccccgaggttgagacatgagaagtgagctc 240
 QY 785 cagtggttgaggaagcacttacaacagagccgttcaagaattatagcaaacaga 844
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 cagtggttgaggaagcacttacaacagagccgttcaagaattatagcaaacaga 300
 QY 845 aaatacctcgcgcctgacgcttctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 904
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 aaatacctcgcgcctgacgcttctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 360
 QY 905 agtcttcaagctctgtctataagcacttcatgtgtgagccagcagtcattctata 964
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 agtcttcaagctctgtctataagcacttcatgtgtgagccagcagtcattctata 420
 QY 965 tggatataatgctctcaagatgcttcatatagtttgcctcgcgcgcgcgcgcgc 1024
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 tggatataatgctctcaagatgcttcatatagtttgcctcgcgcgcgcgcgcgc 480
 QY 1025 tggatataatgctctcaagatgcttcatatagtttgcctcgcgcgcgcgcgc 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 tggatataatgctctcaagatgcttcatatagtttgcctcgcgcgcgcgcgcgc 536

RESULT 3
 AV666882 544 bp mRNA EST 25-AUG-2000
 LOCUS AV666882 Bos taurus adipocyte cell line Bos taurus cDNA clone
 DEFINITION E1ABD21G06 5', mRNA sequence.
 ACCESSION AV666882
 VERSION AV666882.1 GI:9925912
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 544)
 AUTHORS Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and
 Suzuki, H.
 TITLE Bovine cDNA sequencing
 JOURNAL Unpublished (2000)
 COMMENT Contact: Yoshikazu Sugimoto
 Animal Genetics Division
 Shitakawa Institute of Animal Genetics
 Odakura, Nishigo, Nishi-Shitakawa, Fukushima 961-8061, Japan

Tel: 81-248-25-5641
 Fax: 81-248-25-5725
 Email: kazu@icococ.ocn.ne.jp
 Single pass sequencing.
 This clone was obtained from a polyA-deleted cDNA library.
 Location/Qualifiers
 1..544
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone="E1ABD21G06"
 /clone_1id="Bos taurus adipocyte cell line"
 /cell_type="an adipocyte cell line"
 /lab_host="DH10B"
 /note="Vector: pZ11; Site 1: SalI; Site 2: NotI; Poly A
 was deleted from a NotI site"

FEATURES

source

BASE COUNT 165 a 110 c 138 g 131 t

ORIGIN

Query Match 32.1%; Score 519.4; DB 32; Length 544;
 Best Local Similarity 99.6%; Pred. No. 1.8e-122;
 Matches 531; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 450 agacgatagagagaataatgaatgatacagaagaagaatgattcgtcaatgctggt 509
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 12 agacgatagagagaataatgaatgatacagaagaagaatgattcgtcaatgctggt 71
 QY 510 ctcaactgcatgttgtgtgttttggaatataccagacccagaagaagctgtgtc 569
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 72 ctcaactgcatgttgtgtgttttggaatataccagacccagaagaagctgtgtc 131
 QY 570 gataaacccatcaaaaaccagaagttgtgtgtgtgtgtgtgtgtgtgtgtgtgt 629
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 132 gataaacccatcaaaaaccagaagttgtgtgtgtgtgtgtgtgtgtgtgtgtgt 191
 QY 630 tccgagatgcttcaaatgatttaccatgaagaagaatgagacataaagcagaaga 689
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 192 tccgagatgcttcaaatgatttaccatgaagaagaatgagacataaagcagaaga 251
 QY 690 acaagaaga-cgaagaagcagaagcctaagctatcgagatgcttcaacccattaac 748
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 252 acaagaaga-cgaagaagcagaagcctaagctatcgagatgcttcaacccattaac 311
 QY 749 gccccgaggttgagccatgacgaagtggaaggtccagtggtgtgtgtgtgtgtgt 808
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 312 gccccgaggttgagccatgacgaagtggaaggtccagtggtgtgtgtgtgtgtgt 371
 QY 809 acagagccgttcaagaattatgccaagcagaagaataaccgttcgcgcgcgcgcgc 868
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 372 acagagccgttcaagaattatgccaagcagaagaataaccgttcgcgcgcgcgcgc 431
 QY 869 tgcgcgtcgaagatatacattgagcatttggagaggttcttaacgctcgttaaac 928
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 432 tgcgcgtcgaagatatacattgagcatttggagaggttcttaacgctcgttaaac 491
 QY 929 acttcatggttgagccacccagtcattcttataatgataatgataatgtctc 981
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 492 acttcatggttgagccacccagtcattcttataatgataatgataatgtctc 544

RESULT 4
 BF046412 520 bp mRNA EST 10-OCT-2000
 LOCUS BF046412 BP250011A20E3 Soares normalized bovine placenta Bos taurus cDNA
 DEFINITION clone BP250011A20E3 5', mRNA sequence.
 ACCESSION BF046412
 VERSION BF046412.1 GI:10763467
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 520)
 AUTHORS Fukuyama, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and
 Suzuki, H.
 TITLE Bovine cDNA sequencing
 JOURNAL Unpublished (2000)
 COMMENT Contact: Yoshikazu Sugimoto
 Animal Genetics Division
 Shitakawa Institute of Animal Genetics
 Odakura, Nishigo, Nishi-Shitakawa, Fukushima 961-8061, Japan

[illegible]

FEATURES		High quality sequence stop: 479.	
Source	Location/Qualifiers		
	1..479		
	/organism="Bos taurus"		
	/db_xref="taxon:9913"		
	/clone="BP230013B10C8"		
	/sex="female"		
	/lab_host="DH10B"		
	/note="Organ: Placenta; Vector: pT719pac; site_1: EcoRI; site_2: NotI. The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806."		
BASE COUNT	142 a 102 c 122 g 113 t		
ORIGIN			
Query Match	29.5%; Score 477.4; DB 116; Length 479;		
Best Local Similarity	99.8%; Pred. No. 1e-11;		
Matches 478; Conservative	0; Mismatches 1; Indels 0; Gaps 0		
OY	545 acaagccagagaggtctttagttcttqataaacccatcaaaaacccagaagtttggtagca 604		
DB	1 ACACCCAGGAAGGCTCTTTTGTCTGGATAACCCATCAAGAAACCCAGAAAGTGTGGCA 60		
OY	605 qcacgattcagaaggcttggcttccgaqatgatttaagaatggttaccatgaagaag 664		
DB	61 GCACCATTCACAAAGGCTGGCTGGCTCCGAGATGGTTAACATGGTTACCATGAAGAG 120		
OY	665 atgagagataaagaagaagaagaagaagaagaagaagaagaagaagcttaagctat 724		
DB	121 ATGAGAGATTAACGAAGAAAGAAAGAAAGAAAGCAAGCAAGCAAGCTTAAGCTAT 180		
OY	725 cggactggttcaaccatttlaaagcccccagggttctgaacatgaagaaatgaaagctc 784		
DB	181 CGGACTGGTTCAACCCATTAAAGGCCGCCAGTGTGTGACMTAGAGAGTGGAGAGCTC 240		
OY	785 caatgattggaagagcaacttaacaaagacgclcttagacaattattatgccaagaca 844		
DB	241 CAGTGGTGTGGAGAGGCACCTTACACAGAGCCCTCTTACACATATTATTGCGAAGCAGA 300		
OY	845 aaattaccgttgcgtctaacggttttgcgcttggaagataaacttaagctacttggaag 904		
DB	301 AAATTACCGTGCCTCAAGCGTTTTCGCCCTCGGAAGATACATGAGCATTAAGCTGAG 360		
OY	905 agtctctaaagctgcctcaataaagaacttcaatgttggaagcaccacgaatcatcttataca 964		
DB	361 AGTCTTAAGCTCTGCTAATTAAGCACTTCAATGGTGGCCACCCAGACATCTTTATATCA 420		
OY	965 tggtagatgtagtctccagagatgcctttgatagaatttgggtccctctgcgtccctcaaa 1023		
DB	421 TGGTAGATGATGCTCCAGATGATGCTTGTATAGATGGTGCTCTGTGCGCTCTCTTAA 479		
RESULT 7			
AM464433	475 bp	mrna	EST
LOCUS	BP230015B20C5 Soares normalized bovine placenta Bos taurus cDNA		24-FEB-2000
DEFINITION	clone BP230015B20C5 5', mRNA sequence.		
ACCESSION	AM464433		
VERSION	AM464433.1	GI:7034601	
KEYWORDS	EST.		
SOURCE			
ORGANISM	Bos taurus		
	cow.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
	Bovinae; Bovinae; Bos.		
REFERENCE	1 (bases 1 to 475)		
AUTHORS	Levin,H.A., Soares,M.B., Rebelz,M., Pardinias,J., Liu,L. and Larsor,		
	J.H.		
TITLE	Bovine ESTs		
JOURNAL	Unpublished (2000)		

COMMENT

Contact: Lewin, H. A. (Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
640 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 244 5908
Fax: 217 244 5617
Email: h.lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-B534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmed
cross match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
PCR primers

FORWARD: TAATACATGCTGCTATACG
REVERSE: ATTATGCTGCTGTAAG
Insert length: 475 Std Error: 0.00
Plate: BP240015R20 Row: C Column: 5
Seq primer: ACCGATACCAATTCACACAGCA
High quality sequence stop: 475.
Location/Qualifiers

FEATURES

SOURCE

1..475
/organism "bos taurus"
/db_xref "taxon:99134"
/clone "BP240015R20P5"
/clone_1lb "Scars normalized bovine placenta"
/sex "female"
/lab_host "pH10B"
/note "Organic placenta; Vector: p773Hac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was constructed by the
Source Laboratory and it was constructed and normalized
as described by Renaldi, M.F., Lomon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "

BASE COUNT

159 a 101 c 122 g 113 t

ORIGIN

Query Match 29.3% Score 47.4; DB 116; Length 475;

Best Local Similarity 99.8% Pred. No. 1 to 110;
Matches 474; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

545 aacagccaggaagctcttcttgaatataacccatgaagagcagaagatgagatga 604
|||||
1 ATGAGGAGATGAGAGCTCTCTCTCTGATTAATGCAAGAAACGCAAGCTGGGGA 60
|||||
605 gcaagcattcagaagagctggtgcttcagagatgattacacatgattccatgaagaa 664
|||||
61 gcaacattcagaaagcctgctgcttcagacagctttacacatgattacacaaagaa 120
|||||
665 atgagagcattcagaagagagagagagagagagagagagagagagagagagat 724
|||||
121 ATGAGAGATGATTAATGCAAGAAACGCAAGAAACGCAAGCTGGGGA 180
|||||
725 cgaactgattcagacccatttaaacgcccagatcattgacacagacagatggaagcttc 784
|||||
181 cgcacatgctgcaaacatttaaacgcccagctgacacagacagacagacagacagac 240
|||||
785 cgaatggtgagagagagagcttcaaacagagagcttcaaacatgattatgagagagaa 844
|||||
241 cactgctgttcagaaagccttcaaacagagagcttcaaacatgattatgagagagaa 900
|||||
845 aacttaccatcagcctgagcgtttctgcccagagagatgacattgagatgacttgaag 964
|||||
901 AATATATGAGTGTGATGAGCTTTTGGCTGGCAACATGATGACCATTTGAGAG 360
|||||
905 aattcttgaagctgctaatgaagcattcattgagccacccatgactcttataatca 964
|||||
121 ATGAGAGATGATTAATGCAAGAAACGCAAGAAACGCAAGCTGGGGA 180
|||||
121 ACTGCTTAATGCTGCTGATTAATGCAAGAAACGCAAGAAACGCAAGCTGGGGA 420
|||||
965 tgaatgaagatgctcagagagagcttgaatgaatgagctctcagagagctctt 1019
|||||
111 ttt 111
421 TGTATATGATGCTGCTGATTAATGCAAGAAACGCAAGAAACGCAAGCTGGGGA 475

RESULT 8

AV604266 523 bp mRNA EST 30-AUG-2000
AV604266 bos taurus kidney testis bos taurus cDNA clone EIK1015B11
3', mRNA sequence.

AV604266 1 61:9725592
AV604266 EST.

KEYWORDS

EST.

KEYWORDS

SOURCE

ORGANISM

bos taurus

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KEYWORDS


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Db 163 GGATATTAACCTGTGACAGATGCTTCGACAGACAAAGATATATGCTGTAATTA 104
QY 1569 tgcctacattgagcagacattctgaatttgaaagagatattct 1617
Db 103 TGTGTACTTGTGCGAGATGATTTGTGATTTGAGAGAGATATTATCT 55

RESULT 9
AV603267 549 bp mRNA EST 30-AUG-2000
LOCUS AV603267 Bos taurus kidney fetus Bos taurus cDNA clone EIK1015B11
DEFINITION 5', mRNA sequence.
ACCESSION AV603267
VERSION AV603267.1 GI:9725593
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 549)
AUTHORS Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and
Suzuki,H.
TITLE bovine cDNA sequencing
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Shirakawa, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@evora.orn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
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/dev_stage="Fetus"
/lab_host="DH10B"
/note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"
BASE COUNT 154 a 125 c 152 g 118 t
ORIGIN
Query Match 25.7% Score 416: DB 31: Length 549:
Best Local Similarity 97.7%: Pred. No. 66:96:
Matches 422: Conservative 0: Mismatches 10: Indels 0: Gaps 0:
QY 326 caattcacaaatcaacgagatcagaagatgcacattgacattccctccagccctc 365
Db 118 CAGCAATATACAGACAGCTGACGTGCAAGAGCTGCACCTTCCTCCCTCCAGCCCTG 177
QY 386 ctctcagaagaagagctcagtagaacttgatcttgccttllactctaaagagagag 445
Db 178 CTCTGACAGACAGCTGACGTGCAAGAGCTGCACCTTCCTCCCTCCAGAGAGAG 237
QY 446 aagcagagatagaggaataatgaatgtcgaagaaagagatcttgctcaatgctg 505
Db 238 AACGACAGATGAGGAGAAATATCATCTCAAGCAAAAGTCAATTCCTGCAATGCTG 297
QY 506 ttctctcaatctgcatgtgttlltgaagatataatccacagcccaagagctctt 565
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QY 566 tctgataaaccatacaagaaccagaaatgtgtgagcagacagatcagaagagctg 625
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RESULT 10
AK015047 1370 bp mRNA HTC 08-FEB-2001
LOCUS AK015047
DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:493042F06, full insert sequence.
ACCESSION AK015047
VERSION AK015047.1 GI:12853236
KEYWORDS CAP trapper.
SOURCE Mus musculus (strain: c57BL/6J) adult male testis cDNA to mRNA,
clone:lib:RIKEN full-length enriched mouse cDNA library
clone:4930402F06.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Methods Enzymol. 303, 19-44 (1999)
REFERENCE 2 (sites)
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE 3 (sites)
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Kono,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Kikuchi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishino,T.,
Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T.,
Kashiwagi,K., Fujiwara,S., Inoue,K., Tozawa,Y., Izawa,K., Ohara,E.,
Matsuhira,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE 4 (sites)
AUTHORS The RIKEN Genome Exploration Research Group Phase 11 Team and
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5 (bases 1 to 1370)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arikawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M.,
Hanaqaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoaka,T., Hori,F.,
Imocani,K., Ishi,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J.,
Kojima,Y., Kono,H., Konda,M., Koya,S., Kurihara,C., Matsuyama,T.,
Miyazaki,A., Nishi,K., Momura,K., Numaizaki,R., Ono,M., Okazaki,Y.,
Okido,T., Owa,C., Saito,H., Saito,K., Sakai,C., Sakai,K., Sano,H.,
Sasaki,D., Shibata,K., Shibata,Y., Shindagawa,A., Shitaki,T.,
Soabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,K., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,Y.,
Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshitake Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genome Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

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[illegible]

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